

<!--StartFragment-->RESULT 1  
 US-09-110-959A-4  
 ; Sequence 4, Application US/09110959A  
 ; Patent No. 6268197  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schulein, Martin  
 ; APPLICANT: Outtrup, Helle  
 ; APPLICANT: Jorgensen, Per Lina  
 ; APPLICANT: Bjornvad, Mads Eskelund  
 ; TITLE OF INVENTION: Alkaline Xyloglucanase  
 ; FILE REFERENCE: 5206.200-US  
 ; CURRENT APPLICATION NUMBER: US/09/110,959A  
 ; CURRENT FILING DATE: 1998-07-07  
 ; PRIOR APPLICATION NUMBER: 0822/97  
 ; PRIOR FILING DATE: 1997-07-07  
 ; PRIOR APPLICATION NUMBER: 1213/97  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/054,039  
 ; PRIOR FILING DATE: 1997-07-28  
 ; PRIOR APPLICATION NUMBER: 60/063,694  
 ; PRIOR FILING DATE: 1997-10-28  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 537  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus agaradhaerens NCIMB 40482  
 US-09-110-959A-4

*Patent US 6268197*

Query Match 90.1%; Score 2768.5; DB 2; Length 537;  
 Best Local Similarity 95.0%; Pred. No. 7.4e-243;  
 Matches 511; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

Qy	34	EDRVSSSQVDIQSYVADMQPGWNLGNTFDAIGDDETAWGNPRVTRELIEMIADDEGYKSIR	93
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Qy	94	IPVTWQNQMGGSPDYTINEDYIKRVEQVIDWALEEDLYVMLNVHHD SWLWMYDMEHNYDE	153
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Db	60	IPVTWQNQMGGSPDYTINEDYINRVEQAIDWALEEDLYVMLNVHHD SWLWMYDMEHNYDE	119
Qy	154	VMARYTAIWEQLSEKFKNHSHKLMFESVNEPRFTQEWGEIQENHHAYLEDLNKTFYYIVR	213
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Qy	214	ESGGNNVERPLVLPTIETATSQDLLDRLYQTMEDLDDPHLIATVHYYGFWPFSVNIAGYT	273
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Qy	274	RFEQETQQDIIDTFDRVHNTFTANGIPVVLGEFGLLGFDKSTDVQQGEKLFKEFLIHH	333
		:     :     :     :     :     :     :	
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Qy	334	LNERDITHMLWDNGQHLKRETYSWYDQEFHDILKASWEGRSATAESNFIHVKGEPIRDQ	393
		:     :     :     :     :     :     :	
Db	300	LNERDITHMLWDNGQHFNRETYAWYDQEFHDILKASWEGRSATAESNLHVKGDKPIRDQ	359
Qy	394	HIQLYLNGNELTALQAGDESLVLGEDYELAGDVLT LKAGILTRLITPGQLGTNAVITAQF	453
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Db	360	DIQLYLNGNELTALQAGEESLVLGEDYELAGGVLT LKADTLTRLITPGQLGTNAVITAQF	419

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Qy      454 NSGADWRFQLQNVDVPTVENTDGSIIWHFAIPTHFNGDSLATMEAVYANGEYAGPDWTSF 513
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Db      420 NSGADWRFQLQNVDVPTVENTDGSTWHFAIPTHFNGDSLATMEAVYANGEYAGPDWTSF 479
          |||

Qy      514 KEFGAEAFSPNYATGEIIIITEAFFNAVRDDDIHLTFHYWSGETVEYTLRKNGNYVQGRR 571
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Db      480 KEFGAEAFSPNYATGEIIIIEAFFNAVRDDDIHLTFHFWSGETVEYTLRKNGNYVQGRR 537
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